



## SEQUENCE LISTING

Scott, Robert E.

&lt;110&gt;

&lt;120&gt;

cDNA encoding P2P proteins and use of P2P cDNA-derived antibodies and antisense reagents in determining the proliferative potential of normal, abnormal and cancer cells in animals and humans

&lt;130&gt; D6386D

&lt;140&gt; US 09/811,045

&lt;141&gt; 2001-03-16

&lt;150&gt; US 08/801,308

&lt;151&gt; 1997-02-18

&lt;160&gt; 4

&lt;210&gt; 1

&lt;211&gt; 1404

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;223&gt; P2P polypeptide

&lt;400&gt; 1

Met	Met	Glu	Val	Lys	Asp	Pro	Asn	Met	Lys	Gly	Ala	Met	Leu	Thr
								5		10				15
Asn	Thr	Gly	Lys	Tyr	Ala	Ile	Pro	Thr	Ile	Asp	Ala	Glu	Ala	Tyr
								20		25				30
Ala	Ile	Gly	Lys	Lys	Glu	Lys	Pro	Pro	Phe	Leu	Pro	Glu	Glu	Pro
								35		40				45
Ser	Ser	Ser	Glu	Glu	Asp	Asp	Pro	Ile	Pro	Ala	Glu	Leu	Leu	
								50		55				60
Cys	Leu	Ile	Cys	Lys	Asp	Ile	Met	Thr	Asp	Ala	Val	Val	Ile	Pro
								65		70				75
Cys	Cys	Gly	Asn	Ser	Ser	Cys	Asp	Glu	Cys	Ile	Arg	Thr	Thr	Leu
								80		85				90
Leu	Glu	Ser	Asp	Lys	His	Thr	Cys	Pro	Thr	Cys	His	Gln	Asn	Asp
								95		100				105
Val	Ser	Pro	Asp	Ala	Leu	Ile	Ala	Asn	Lys	Phe	Leu	Arg	Gln	Ala
								110		115				120
Val	Asn	Asn	Phe	Lys	Asn	Glu	Thr	Gly	Tyr	Thr	Lys	Arg	Leu	Arg
								125		130				135
Lys	Gln	Leu	Pro	Pro	Phe	Leu	Phe	Leu	Val	Pro	Pro	Pro	Arg	Pro
								140		145				150
Leu	Ser	Gln	Arg	Asn	Leu	Gln	Pro	Arg	Ser	Arg	Ser	Pro	Ile	Leu
								155		160				165

Arg	Gln	Gln	Asp	Pro	Val	Val	Phe	Arg	Tyr	Thr	Val	Ser	Pro	Thr
				170					175					180
Cys	Ser	Asp	Thr	Lys	Thr	Ala	Gly	Ser	Cys	Ser	Asp	Ser	Gly	Thr
				185					190					195
Leu	Ser	Arg	Leu	Pro	Ala	Pro	Ser	Ile	Ser	Ser	Leu	Thr	Ser	Asn
				200					205					210
Gln	Ser	Ser	Leu	Ala	Pro	Pro	Val	Ser	Gly	Asn	Pro	Ser	Ser	Ala
				215					220					225
Pro	Ala	Pro	Val	Pro	Asp	Ile	Thr	Ala	Thr	Val	Ser	Ile	Ser	Val
				230					235					240
His	Ser	Glu	Lys	Ser	Asp	Gly	Pro	Phe	Arg	Asp	Ser	Asp	Asn	Lys
				245					250					255
Leu	Leu	Pro	Ala	Ala	Ala	Leu	Thr	Ser	Glu	His	Ser	Lys	Gly	Ala
				260					265					270
Ser	Ser	Ile	Ala	Ile	Thr	Ala	Leu	Met	Glu	Glu	Lys	Gly	Val	Pro
				275					280					285
Gly	Thr	Ser	Pro	Trp	Asn	Ser	Ile	Phe	Val	Gly	Gln	Ser	Leu	Leu
				290					295					300
His	Gly	Gln	Leu	Ile	Pro	Thr	Thr	Gly	Pro	Val	Arg	Ile	Asn	Ala
				305					310					315
Ala	Arg	Pro	Gly	Gly	Gly	Arg	Pro	Gly	Trp	Glu	His	Ser	Asn	Lys
				320					325					330
Leu	Gly	Tyr	Leu	Val	Ser	Pro	Pro	Gln	Gln	Ile	Arg	Arg	Gly	Glu
				335					340					345
Arg	Ser	Cys	Tyr	Arg	Ser	Ile	Asn	Arg	Gly	Arg	His	His	Ser	Glu
				350					355					360
Arg	Ser	Gln	Arg	Thr	Gln	Ser	Pro	Ser	Leu	Pro	Ala	Thr	Pro	Cys
				365					370					375
Phe	Val	Pro	Val	Pro	Pro	Pro	Pro	Leu	Tyr	Pro	Pro	Pro	Pro	His
				380					385					390
Thr	Leu	Pro	Leu	Pro	Pro	Gly	Val	Pro	Pro	Pro	Gln	Phe	Ser	Pro
				395					400					405
Gln	Phe	Pro	Ser	Ser	Gln	Pro	Pro	Thr	Ala	Gly	Tyr	Ser	Val	Pro
				410					415					420
Pro	Pro	Gly	Phe	Pro	Pro	Ala	Pro	Ala	Asn	Ile	Ser	Thr	Ala	Cys
				425					430					435
Phe	Ser	Pro	Gly	Val	Pro	Thr	Ala	His	Ser	Asn	Thr	Met	Pro	Thr
				440					445					450
Thr	Gln	Ala	Pro	Leu	Leu	Ser	Arg	Glu	Glu	Phe	Tyr	Arg	Glu	Gln
				455					460					465
Asn	Asp	Lys	Gly	Arg	Glu	Ser	Lys	Phe	Pro	Tyr	Ser	Gly	Ser	Ser
				470					475					480
Tyr	Ser	Arg	Ser	Ser	Tyr	Thr	Asp	Ser	Ser	Gln	Gly	Leu	Ala	Gln
				485					490					495
His	Ile	His	Ala	Leu	Thr	Leu	Ser	Pro	Ser	Ala	Ala	His	Thr	Leu
				500					505					510
Asp	Leu	Leu	His	Asp	His	Pro	His	Pro	Pro	Glu	Glu	Ala	Glu	Ala
				515					520					525
Arg	Ser	Ala	Met	Ile	Val	His	Met	Pro	Asp	Leu	Met	Asp	Ile	Ala
				530					535					540
His	Ala	Arg	Ser	Arg	Ser	Pro	Pro	Tyr	Arg	Arg	Tyr	Arg	Ser	Arg
				545					550					555

Ser	Arg	Ser	Pro	Pro	Glu	Phe	Arg	Gly	Gln	Ser	Pro	Thr	Lys	Arg
					560				565					570
Asn	Val	Pro	Arg	Glu	Glu	Lys	Glu	Arg	Glu	Tyr	Phe	Asn	Arg	Tyr
					575				580					585
Arg	Glu	Val	Pro	Pro	Pro	Tyr	Asp	Ile	Lys	Ala	Tyr	Tyr	Gly	Arg
					590				595					600
Ser	Val	Asp	Phe	Arg	Asp	Pro	Phe	Glu	Lys	Glu	Arg	Tyr	Arg	Glu
					605				610					615
Trp	Glu	Arg	Lys	Tyr	Arg	Glu	Trp	Tyr	Glu	Lys	Tyr	Tyr	Lys	Gly
					620				625					630
Tyr	Ala	Val	Gly	Ala	Gln	Pro	Arg	Pro	Ser	Ala	Asn	Arg	Glu	Asp
					635				640					645
Phe	Ser	Pro	Glu	Arg	Leu	Leu	Pro	Leu	Asn	Ile	Arg	Asn	Ser	Pro
					650				655					660
Phe	Thr	Arg	Gly	Arg	Arg	Glu	Asp	Tyr	Ala	Ala	Gly	Gln	Ser	His
					665				670					675
Arg	Asn	Arg	Asn	Leu	Gly	Gly	Asn	Tyr	Pro	Glu	Lys	Leu	Ser	Thr
					680				685					690
Arg	Asp	Ser	His	Asn	Ala	Lys	Asp	Asn	Pro	Lys	Ser	Lys	Glu	Lys
					695				700					705
Glu	Ser	Glu	Asn	Val	Pro	Gly	Asp	Gly	Lys	Gly	Asn	Lys	His	Lys
					710				715					720
Lys	His	Arg	Lys	Arg	Arg	Asn	Glu	Glu	Lys	Gly	Glu	Glu	Ser	Glu
					725				730					735
Ser	Phe	Leu	Asn	Pro	Glu	Leu	Leu	Glu	Thr	Ser	Arg	Lys	Cys	Arg
					740				745					750
Gly	Ser	Ser	Gly	Ile	Asp	Glu	Thr	Lys	Thr	Asp	Thr	Leu	Phe	Val
					755				760					765
Leu	Pro	Ser	Arg	Asp	Asp	Ala	Thr	Pro	Val	Arg	Asp	Glu	Pro	Met
					770				775					780
Asp	Ala	Glu	Ser	Ile	Thr	Phe	Lys	Ser	Val	Ser	Asp	Lys	Asp	Lys
					785				790					795
Arg	Glu	Lys	Asp	Lys	Pro	Lys	Val	Lys	Ser	Asp	Lys	Thr	Lys	Arg
					800				805					810
Lys	Ser	Asp	Gly	Ser	Ala	Thr	Ala	Lys	Lys	Asp	Asn	Val	Leu	Lys
					815				820					825
Pro	Ser	Lys	Gly	Pro	Gln	Glu	Lys	Val	Asp	Gly	Asp	Arg	Glu	Lys
					830				835					840
Ser	Pro	Arg	Ser	Glu	Pro	Pro	Leu	Lys	Lys	Ala	Lys	Glu	Glu	Ala
					845				850					855
Thr	Lys	Ile	Asp	Ser	Val	Lys	Pro	Ser	Ser	Ser	Ser	Gln	Lys	Asp
					860				865					870
Glu	Lys	Val	Thr	Gly	Thr	Pro	Arg	Lys	Ala	His	Ser	Lys	Ser	Ala
					875				880					885
Lys	Asp	Thr	Arg	Arg	Gln	Ser	Gln	Pro	Arg	Thr	Arg	Arg	Ser	Lys
					890				895					900
Arg	Thr	Val	Pro	Lys	Thr	Ser	Ser	Gln	Lys	Ser	Gln	Pro	Val	Arg
					905				910					915
Thr	Arg	Arg	Pro	Arg	Ser	Leu	Arg	Lys	Ile	Asn	Tyr	Leu	Ile	Ala
					920				925					930
Arg	Glu	Lys	Asn	Glu	Arg	Glu	Lys	Arg	Lys	Lys	Ser	Val	Asp	Lys
					935				940					945

Asp	Phe	Glu	Ser	Ser	Ser	Met	Lys	Ile	Ser	Lys	Val	Glu	Gly	Thr
						950			955					960
Glu	Ile	Val	Lys	Pro	Ser	Pro	Lys	Arg	Lys	Met	Glu	Gly	Asp	Val
						965			970					975
Glu	Lys	Leu	Glu	Arg	Thr	Pro	Glu	Lys	Asp	Lys	Ile	Ala	Ser	Ser
						980			985					990
Thr	Thr	Pro	Ala	Lys	Lys	Ile	Lys	Leu	Asn	Arg	Glu	Thr	Gly	Lys
						995			1000					1005
Lys	Ile	Gly	Asn	Ala	Glu	Asn	Ala	Ser	Thr	Thr	Lys	Glu	Pro	Ser
						1010			1015					1020
Glu	Lys	Leu	Glu	Ser	Thr	Ser	Ser	Lys	Ile	Lys	Gln	Glu	Lys	Val
						1025			1030					1035
Lys	Gly	Lys	Ala	Lys	Arg	Lys	Val	Ala	Gly	Ser	Glu	Gly	Ser	Ser
						1040			1045					1050
Ser	Thr	Leu	Val	Asp	Tyr	Thr	Ser	Thr	Ser	Ser	Thr	Gly	Gly	Ser
						1055			1060					1065
Pro	Val	Arg	Lys	Ser	Glu	Glu	Lys	Thr	Asp	Thr	Lys	Arg	Thr	Val
						1070			1075					1080
Ile	Lys	Thr	Met	Glu	Glu	Tyr	Asn	Asn	Asp	Asn	Thr	Ala	Pro	Ala
						1085			1090					1095
Glu	Asp	Val	Ile	Ile	Met	Ile	Gln	Val	Pro	Gln	Ser	Lys	Trp	Asp
						1100			1105					1110
Lys	Asp	Asp	Phe	Glu	Ser	Glu	Glu	Glu	Asp	Val	Lys	Thr	Thr	Gln
						1115			1120					1125
Pro	Ile	Gln	Ser	Val	Gly	Lys	Pro	Ser	Ser	Ile	Ile	Lys	Asn	Val
						1130			1135					1140
Thr	Thr	Lys	Pro	Ser	Ala	Thr	Ala	Lys	Tyr	Thr	Glu	Lys	Ser	
						1145			1150					1155
Glu	Gln	Pro	Glu	Lys	Leu	Gln	Lys	Leu	Pro	Lys	Glu	Ala	Ser	His
						1160			1165					1170
Glu	Leu	Met	Gln	His	Glu	Leu	Arg	Ser	Ser	Lys	Gly	Ser	Ala	Ser
						1175			1180					1185
Ser	Glu	Lys	Gly	Arg	Ala	Lys	Asp	Arg	Glu	His	Ser	Gly	Ser	Glu
						1190			1195					1200
Lys	Asp	Asn	Pro	Asp	Lys	Arg	Lys	Ser	Gly	Ala	Gln	Pro	Asp	Lys
						1205			1210					1215
Glu	Ser	Thr	Val	Asp	Arg	Leu	Ser	Glu	Gln	Gly	His	Phe	Lys	Thr
						1220			1225					1230
Leu	Ser	Gln	Ser	Ser	Lys	Glu	Thr	Arg	Thr	Ser	Glu	Lys	His	Glu
						1235			1240					1245
Ser	Val	Arg	Gly	Ser	Ser	Asn	Lys	Asp	Phe	Thr	Pro	Gly	Arg	Asp
						1250			1255					1260
Lys	Lys	Val	Asp	Tyr	Asp	Ser	Arg	Asp	Tyr	Ser	Ser	Ser	Lys	Arg
						1265			1270					1275
Arg	Asp	Glu	Arg	Gly	Glu	Leu	Ala	Arg	Arg	Lys	Asp	Ser	Pro	Pro
						1280			1285					1290
Arg	Gly	Lys	Glu	Ser	Leu	Ser	Gly	Gln	Lys	Ser	Lys	Leu	Arg	Glu
						1295			1300					1305
Glu	Arg	Asp	Leu	Pro	Lys	Lys	Gly	Ala	Glu	Ser	Lys	Lys	Ser	Asn
						1310			1315					1320
Ser	Ser	Pro	Pro	Arg	Asp	Lys	Lys	Pro	His	Asp	His	Lys	Ala	Pro
						1325			1330					1335

Tyr	Glu	Thr	Lys	Arg	Pro	Cys	Glu	Glu	Thr	Lys	Pro	Val	Asp	Lys
							1340		1345					1350
Asn	Ser	Gly	Lys	Glu	Arg	Glu	Lys	His	Ala	Ala	Glu	Ala	Arg	Asn
							1355		1360					1365
Gly	Lys	Glu	Ser	Ser	Gly	Ala	Asn	Cys	His	Val	Tyr	Leu	Thr	Arg
							1370		1375					1380
Gln	Thr	Leu	Pro	Trp	Arg	Arg	Ser	Trp	Leu	Leu	Gly	Arg	Trp	Arg
							1385		1390					1395
Arg	Ala	Pro	Ser	Ser	Arg	Asn	Pro	Ser						
							1400							

<210> 2  
<211> 5173  
<212> DNA  
<213> Unknown

<220>

<221> cDNA  
<223> P2P cDNA

<400> 2

agg tcc accca cttccatctt acac ctg ctt tcgtt gtgg aaac ctgg tc attat attaa 60  
gaatt gcca acaa atggga taaga acttt gaat ctgg tc ctaggat caa aaag agc act 120  
ggaatt ccta gaag ttat gatg gaag tg aaag atc cta acatg aaaa agg tgca atg ctt 180  
acca acactg gaaa atatgc aata ccact atag atgc ag ggcc tata tc aatc ggg aag 240  
aaag agaa ac cacc tt ctt acca gaggg ccat catcat cttc aga aaga agat gat cct 300  
atccc agc agc agt ctt gtt ctc atc tgc aaag acatca tgact gat gc tgg tca ttt 360  
ccct gct gtg gaa ac agttc atgt gat gaa tgtata aaga cgac act tttt ggag tc agat 420  
aaac ataca at gtcc aac atg tc acc aaaa at gat gtt ctc ctg atg cttt aatt gcca ac 480  
aa gtttt tac gac agg ctgt taata acttt aaaa atg aaaa ctgg ctata cca aac acg aca 540  
cgaaa acagt tac ctcc attt tttt tttt gtacc accac caa gacc act cagt cag cgg 600  
aac ctac agc ctc tagt tag atc tcc aata cta aga cagc agg atc tttt tttt tttt tttt 660  
ta ca ctg tct cgc tcc gata ct aag acagc ag gat ctc tgg tag tgatt cagg t 720  
acact gtc tc gc ct ac ctgc tcc gtc tata tctt catt aa ctt cta atca gtctt cttt 780  
gccc ctcc tgg tttt tttt tttt gtc cag ctc cag tacc tga tata act gca 840  
acc gtc tca ttc agt ctc ctt cttt tttt tttt tttt tttt tttt tttt tttt tttt tttt 900  
aaattt attgc cag ctg ccgc ctt tac atca gaac attt cttt tttt tttt tttt tttt tttt 960  
attact gtc ttat gga aaaa agggta ccagg tacc gtc ctgg aaaa ctcc atctt tttt tttt 1020  
gtt ggac agt catt attaca tgg ac agttt atccc acat cttt tttt tttt tttt tttt tttt 1080  
gct gtc gtc cagg tgg gg ccgg ccagg cc tgg gac tttt tttt tttt tttt tttt tttt tttt 1140  
gttt ctcc ac caca aat tag aag agga gaa aag ct gtt ac aga ag tata aac ccgc 1200  
ggc gac acc ac agc gaac g atc ac aca gagg act caa agcc catc ac ttcc tttt tttt 1260  
tgctt tgc ccgtt ccacc acct cttt tttt tttt tttt tttt tttt tttt tttt tttt tttt 1320  
cctcc aggtg tac ctcc tcc ac agt tttt tttt tttt tttt tttt tttt tttt tttt tttt 1380  
gcaggatata gtgt ccctcc tccaggatt cc acc ag ctc ctg cca atat atca ac agt 1440  
tgctttt cacc cagg tgg tcc cact gccc cat tca aat acca tgcc caca ac aca agc acct 1500  
ctttt gtc ca ggg aaaa ctat aga gagg caaa ac gaca aagg aagaga gtct aaattt 1560  
ccctat agt ggt ctc atcgta ttca aaga agt tcata act g act caa gtc aggt ctgg ct 1620  
caac acat tc ac gtc tttt ac tca gtc tttt tttt tttt tttt tttt tttt tttt tttt 1680  
gatcatcccc atc tcc aaga agagg cagag gca agat ctg caat gat tgg ttc acat gcca 1740  
gatctcatgg atat gcca tgct taggtca aggt cac ttc cctat agac g atat gctca 1800

cggtccagat ctcctccaga atttagggga cagtctcca ctaaacgtaa tgtacctcga 1860  
gaagagaaaag aacgtgagta ttttaataga tacagagaag ttccacccccc ttatgacatc 1920  
aaagcctatt atggcgagg tgcactt agagacccat ttgagaaaaga acgctaccgg 1980  
gaatgggaaa ggaaataccg agagtggat gagaagtact acaaaggta cgcggtgga 2040  
gctcaaccctt gaccctcagc caatagagag gactttctc cagagagact cttaccttt 2100  
aatatcagaa attcaccctt cacaagaggc cgccagagaag actatgctgc tggacaaagt 2160  
catagaaata gaaatctagg tggcaactat ccagaaaagc tttcaacaag ggacagtac 2220  
aatgcaaaaag ataatccaaa atcgaaggag aaggagagtg agaatgttcc aggagacggc 2280  
aaaggaaaca agcataagaa acacaggaaa cgaagaaacg aagaaaaggg ggaagagagt 2340  
gagagcttcc tgaacccaga gctactggag acgtctagga aatgcagggg atcgtcaggg 2400  
attgatgaaa cgaagacaga tacactgtt gttctccaa gcagagacga tgctcacct 2460  
gttagggatg agccaatggc cgccagaatcg atcacccatc agtcagttc tgacaaagac 2520  
aagagggaaa aggataagcc aaaagtaaaa agtgacaaga ccaaaccggaa aagtgacggg 2580  
tctgctacag ccaagaaaga caatgttta aaacccctca aaggacctca agaaaaggta 2640  
gatggagacc gtggaaaagtc tcctcggtct gagccgccac tcaaaaaaagc caaagaggag 2700  
gctacaaaga ttgactctgt aaaacccccc tcgtcttc agaaggatga gaaggtcact 2760  
ggaaccccta gaaaagccca ttctaaatct gcaaaagaca ccaggaggca aagccagcca 2820  
aggacgagaa ggtcaaaaag gactgttcca aagacatcaa gtcagaaaag ccagccagta 2880  
aggacgagaa ggcagaagaag cctgagaaaa ataaactact tgatagcaag ggagaaaaac 2940  
gaaagagaaa aacggaagaa gagtgtagat aaagatttg agtcgttcc aatgaaaatc 3000  
tctaaagtag aagaacaga aatagtgaaa ccatcaccaa aacggaaaat ggaaggtgat 3060  
gttggaaaagc tggaaaaggac cccagaaaag gacaagattt catcatcaac tactccagcc 3120  
aaaaaaaaatca aactcaacag agaaactggc aaaaaattt gaaatgcaga aaatgcac 3180  
actacaaaag aaccctctga aaaattggag tcaacatcta gcaaaatcaa acaggaaaaa 3240  
gtcaaggggaa aggccaaacg gaaagtagct gggtcggaaag gctccagctc cacgcttgt 3300  
gattacacca gtacaagttc aactggaggc agtcctgtga gggaaatctga agaaaagaca 3360  
gatacaaagc gaacagtcat taaaactatg gaggaatata ataatgataa cacagctcct 3420  
gctgaagatg ttataattt gatccagggtt cctcagttca aatgggataa agatgactt 3480  
gagtctgaag aagaagatgt taaaaccaca caacctatac agagttagg gaaaccatcg 3540  
agtattataa aaaatgtcact tactaagcc tcggctacgg ctaagtacac cgagaaggaa 3600  
agcgagcagc ccgagaaaact gcagaagctt cccaggagg cgagccacga gctgtcgc 3660  
cacgagctca ggagctcaaa gggcagtgcg tccagtgaga agggcagagc caaggaccgg 3720  
gagcactcag ggtcgagaaa ggacaaccct gacaagagga agagcgtgc ccagccagac 3780  
aaggagagca ctgtggaccg cctgagtgag cagggacatt ttaagactct ctctcagtct 3840  
tccaaagaga ccaggacttc agagaagcac gagtctgttc gtggttctc aaataaaagac 3900  
ttcactcctg gtagagacaa gaaagtggac tacgacagca gggattattc cagttccaag 3960  
cgaagagacg agagaggta attagcaagg agaaaagact ctcctccccg gggcaaagag 4020  
tctctgtctg ggcagaaaag caagctgagg gaggagagag atttacctaa aaaggggggcc 4080  
gagtcaaaaa aaagtaattt tagccccca agagacaaaaa agcctcatga tcataaaagcc 4140  
ccctacgaaa ctaaacgccc atgtgaagag acaaagcctg tagataaaaaa ctctggaaag 4200  
gagcgggaga agcatgctgc tgaagctgc aatggaaaag agtccagtg tgcaaactgc 4260  
catgtataacc taacccgcca gaccctccca tggagaagga gctggctgct gggcaggtgg 4320  
agaagagcgc cgtcaagccg aaaccccagc tgagccattc ctcgaggctt tcctctgacc 4380  
tgaccgggaa gacgaacgag gcaggcttg aaccagatta taatgagagc gacagtgaga 4440  
gtaatgtgtc tgtgaaggaa gaagaagctg ttgccagtt ctccaaggac ttgaaagaga 4500  
aaacaacaga gaaagcgaaa gagagctga ctgtagcaac ggccagccag ccaggtcgc 4560  
acaggagcca gagccaaagt agcccaagt tagtcagtag agtcatagcc ttcggagcca 4620  
gacccgaagc cacagcagca gtgccagctc agccggaagg ccaggacagc aaaaagaaga 4680  
agaagaagaa ggagaagaaa aacgacaaga agcataaaaaa gcacaagaag cacaagaagc 4740  
acgcaggccg acggcgacgt ggagaagagc cagaaacaca aacacaagaa gaagaaggcc 4800  
aagaagaaca aagacaagga gaaggagaaa gatgaccaaaa aagtgagatc tgcactgtg 4860  
tgaaggacgg atgtgttaat tgacttaatt actaagtcat ctgttataa ttctgttata 4920

atgtaaaagag attccagcct tgtaaataat gaatggaaga ccctgtgctg cactaaaaag 4980  
tatttgctgc ttgattattt cattttaca tcagagctt ataacgaact tttgtacaga 5040  
attgtgagggt gtgaccatgg aacagtgaga gttttgcta gggcctatta ttttaacca 5100  
ccattaattt gttgggtgg agtttactgt actgtgaaat tttcacattt gaatttttt 5160  
aattgcctgg caa 5173

<210> 3  
<211> 16  
<212> DNA  
<213> Unknown

<220>

<221> primer\_bind  
<223> P2P antisense oligonucleotide

<400> 3  
cagcaggagc tgtgtt 16

<210> 4  
<211> 16  
<212> DNA  
<213> Unknown

<220>

<221> primer\_bind  
<223> P2P sense oligonucleotide

<400> 4  
ctactaagcc atcggc 16